

SCORE Search Results Details for Application 10 20081104_154455_us-10-578-7

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This page gives you Search Results detail for the Application 10578781 and Search Result 2008110

GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2008, 17:10:38 ; Search time 1527 Seconds
(without alignments)
45700.779 Million cell updates/sec

Title: US-10-578-781-1
Perfect score: 756
Sequence: 1 atgggtgccgatcaaaaa.....aggagcaaattgaacattag 756

Scoring table: IDENTIFY_NUC
Gapop 10.0, Gapext 1.0

Searched: 11299264 seqs, 46154159321 residues

Total number of hits satisfying chosen parameters: 22598528

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl : *

- 1: gb_env: *
- 2: gb_pat: *
- 3: gb_ph: *
- 4: gb_pl: *
- 5: gb_pr: *
- 6: gb_ro: *
- 7: gb_sts: *
- 8: gb_sy: *
- 9: gb_un: *
- 10: gb_vi: *
- 11: gb_ov: *
- 12: gb_in: *
- 13: gb_om: *
- 14: gb_ba: *
- 15: gb_htg1: *
- 16: gb_htg2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
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1	756	100.0	756	2	DD160143	DD160143 Novel Bre
2	756	100.0	756	2	DI 115290	DI 115290 Novel Bre
3	366.2	48.4	1746	14	BACSPQI	L47358 Paeni bacill
4	363.2	48.0	1799	14	Z54161	Z54161 B. coagulans
5	361.6	47.8	3701	14	AJ704768	AJ704768 Bacillus
c 6	361.6	47.8	110000	14	CP000560_22	Continuation (23 o
c 7	354.6	46.9	110000	14	CP000813_21	Continuation (22 o
c 8	353.6	46.8	110000	14	CP000557_23	Continuation (24 o
9	348.4	46.1	110000	14	AP006627_19	Continuation (20 o
10	345.6	45.7	864	14	BACSPQ2A	MI5744 B. subtilis
c 11	345.6	45.7	204537	14	Z99116	Z99116 Bacillus su
12	345.6	45.7	282700	14	BACJH642	D84432 Bacillus su
13	343	45.4	110000	14	BA000004_16	Continuation (17 o
c 14	342	45.2	110000	14	CP000764_28	Continuation (29 o
15	339.6	44.9	1920	14	X63757	X63757 B. megateriu
c 16	338.8	44.8	110000	14	AE016877_40	Continuation (41 o
c 17	338.2	44.7	110000	14	AE017194_38	Continuation (39 o
c 18	333.8	44.2	110000	14	BA000043_23	Continuation (24 o
c 19	333.4	44.1	110000	14	CP000903_39	Continuation (40 o
c 20	330.2	43.7	110000	14	CP000001_39	Continuation (40 o
c 21	330.2	43.7	110000	14	CP000485_39	Continuation (40 o
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c 23	330.2	43.7	110000	14	AE017225_39	Continuation (40 o
c 24	330.2	43.7	110000	14	AE017334_39	Continuation (40 o
c 25	330.2	43.7	110000	14	AE017355_38	Continuation (39 o
c 26	330.2	43.7	110000	14	AE017355_39	Continuation (40 o
27	329.4	43.6	1777	14	BACSPQI B	L47360 Bacillus st
28	328.6	43.5	759	8	EF039064	EF039064 Synthetic
29	323.2	42.8	2073	14	BACSPQ2AB	MI7643 B. subtilis
30	317	41.9	1907	14	BACSPQI A	M25260 Bacillus li
c 31	317	41.9	110000	14	CP000002_24	Continuation (25 o
c 32	317	41.9	110000	14	AE017333_24	Continuation (25 o
c 33	316.2	41.8	110000	14	BA000028_18	Continuation (19 o
34	273.4	36.2	665	2	AR805946	AR805946 Sequence
35	273.4	36.2	665	2	AX437345	AX437345 Sequence
36	254.6	33.7	1857	14	BACSPQI A	L47359 Bacillus sp
c 37	253.4	33.5	110000	14	CP000232_15	Continuation (16 o
38	244.2	32.3	110000	14	CP000817_17	Continuation (18 o
39	244.2	32.3	110000	14	CP000817_18	Continuation (19 o
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41	234.2	31.0	110000	14	CP000612_11	Continuation (12 o
42	233.2	30.8	110000	14	CP000232_08	Continuation (9 of
c 43	231	30.6	110000	14	CP000930_04	Continuation (5 of
c 44	224.6	29.7	110000	14	AP008230_32	Continuation (33 o
45	223.6	29.6	110000	14	CP000930_20	Continuation (21 o

ALIGNMENTS

RESULT 1
 DD160143
 LOCUS DD160143 756 bp DNA linear PAT 23-NOV-2005
 DEFINITION Novel Brevibacillus choshinensis and Producing Method of Protein by Using Thereof as Host.
 ACCESSION DD160143
 VERSION DD160143.1 GI: 83960018
 KEYWORDS WO 2005045005- A/1.
 SOURCE Brevibacillus choshinensis
 ORGANISM Brevibacillus choshinensis
 Bacteria; Firmicutes; Bacillales; Paeni bacillaceae; Brevibacillus.
 REFERENCE 1 (bases 1 to 756)
 AUTHORS Hanagata, H. and Nishijyo, T.
 TITLE Novel Brevibacillus choshinensis and Producing Method of Protein by Using Thereof as Host
 JOURNAL Patent: WO 2005045005- A 1 19- MAY- 2005;
 Higeta Shoyu Co Ltd
 COMMENT OS Brevibacillus choshinensis

PN WD 2005045005- A/ 1
 PD 19- MAY- 2005
 PF 08- NOV- 2004 WD 2004JP016912
 PR 11- NOV- 2003 JP 03P 381606
 PI hi roshi hanagat a, takayuki ni shi j yo
 CC
 FH Key Location/ Qual i f i e r s.

FEATURES
 source Location/ Qual i f i e r s
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 / or gani sm=" Brevi baci l l us choshi nensi s"
 / mol _t ype=" unassi gned DNA"
 / db_ xref =" t axon: 54911"

ORI G I N

Query Match 100. 0% Score 756; DB 2; Length 756;
 Best Local Si mi l ari t y 100. 0% Pred. No. 6. 7e- 232;
 Mat ches 756; Conservati ve 0; M smat ches 0; I ndel s 0; Gaps 0;

Qy	1	ATGGGTGCGATATCAAAAATGCGAGTCAACCATTTCTGACCAATGACCAAGTGAAAGAT	60
Db	1	ATGGGTGCGATATCAAAAATGCGAGTCAACCATTTCTGACCAATGACCAAGTGAAAGAT	60
Qy	61	TTGATAGCCAAGAGCCAAGCTGGCGATACGGATGCACGTGAGCTTCTCGTGAATAGCAAT	120
Db	61	TTGATAGCCAAGAGCCAAGCTGGCGATACGGATGCACGTGAGCTTCTCGTGAATAGCAAT	120
Qy	121	ATCAGACTGGTCTGGTCCGTGGTCCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGAT	180
Db	121	ATCAGACTGGTCTGGTCCGTGGTCCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGAT	180
Qy	181	TTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACAAGTTCGATCTTTTGTAC	240
Db	181	TTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACAAGTTCGATCTTTTGTAC	240
Qy	241	GATGTGAGATTTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCACGCTTTTTTG	300
Db	241	GATGTGAGATTTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCACGCTTTTTTG	300
Qy	301	CGCGATGACGGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGG	360
Db	301	CGCGATGACGGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGG	360
Qy	361	CGATCAAAGGATGAATTGTACAAGCAATTCGGCGGTGCCCCACGATCGCAGAAAGTGGCA	420
Db	361	CGATCAAAGGATGAATTGTACAAGCAATTCGGCGGTGCCCCACGATCGCAGAAAGTGGCA	420
Qy	421	GAAACAGTGGGAATCACGCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCCT	480
Db	421	GAAACAGTGGGAATCACGCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCCT	480
Qy	481	TCCTCCATCCATGAGACCGTTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAG	540
Db	481	TCCTCCATCCATGAGACCGTTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAG	540
Qy	541	ATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGC	600
Db	541	ATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGC	600
Qy	601	AGGCTGAGCGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAG	660
Db	601	AGGCTGAGCGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAG	660
Qy	661	TCTGAGGTAGCAGAGCGTCTAGGGATTTTCGAGGTCCAGGTCTCGGTCTGGAAAAGCGT	720
Db	661	TCTGAGGTAGCAGAGCGTCTAGGGATTTTCGAGGTCCAGGTCTCGGTCTGGAAAAGCGT	720
Qy	721	ATCCTGCTAACGATCAAGGAGCAAATTGAACATTAG	756
Db	721	ATCCTGCTAACGATCAAGGAGCAAATTGAACATTAG	756

RESULT 2
 DI 115290
 LOCUS DI 115290 756 bp DNA linear PAT 21-FEB-2008
 DEFINITION Novel *Brevibacillus choshinensis* and Producing Method of Protein by Using Thereof as Host.
 ACCESSION DI 115290
 VERSION DI 115290.1 GI:168311716
 KEYWORDS KR 1020067008845- A/1.
 SOURCE *Brevibacillus choshinensis*
 ORGANISM *Brevibacillus choshinensis*
 Bacteria; Firmicutes; Bacillales; Paenibacillaceae; *Brevibacillus*.
 REFERENCE 1 (bases 1 to 756)
 AUTHORS Hanagata, H. and Nishijyo, T.
 TITLE Novel *Brevibacillus choshinensis* and Producing Method of Protein by Using Thereof as Host
 JOURNAL Patent: KR 1020067008845- A 1 08-MAY-2006;
 COMMENT PN KR 1020067008845- A/1
 PD 2006-05-08
 PA HANAGATA, H., NISHIJYO, T.
 TY DNA
 OS *Brevibacillus choshinensis*
 CO.
 FEATURES Location/Qualifiers
 source 1..756
 /organism="Brevibacillus choshinensis"
 /mol_type="unassigned DNA"
 /db_xref="taxon:54911"

ORIGIN

Query Match 100.0% Score 756; DB 2; Length 756;
 Best Local Similarity 100.0% Pred. No. 6.7e-232;
 Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGGGTGCGGATATCAAAAATGCGAGTCAACCATTCTGACCAATGACCAAGTGAAAGAT 60
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Qy     61 TTGATAGCCAAGAGCCAAGCTGGCGATACGGATGCACGTGAGCTTCTCGTGAATAGCAAT 120
        |||
Db     61 TTGATAGCCAAGAGCCAAGCTGGCGATACGGATGCACGTGAGCTTCTCGTGAATAGCAAT 120
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Qy    121 ATCAGACTGGTCTGGTCCGTCCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGAT 180
        |||
Db    121 ATCAGACTGGTCTGGTCCGTCCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGAT 180
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Qy    181 TTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACAAGTTCGATCTTTTGTAC 240
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Db    181 TTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACAAGTTCGATCTTTTGTAC 240
        |||

Qy    241 GATGTGAGATTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCAACGCTTTTGTG 300
        |||
Db    241 GATGTGAGATTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCAACGCTTTTGTG 300
        |||

Qy    301 CCGGATGACGGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGG 360
        |||
Db    301 CCGGATGACGGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGG 360
        |||

Qy    361 CGATCAAAGGATGAATTGTACAAGCAATTCGGCGGTGCCCCACGATCGCAGAAAGTGGCA 420
        |||
Db    361 CGATCAAAGGATGAATTGTACAAGCAATTCGGCGGTGCCCCACGATCGCAGAAAGTGGCA 420
        |||

Qy    421 GAAGCAGTGGGAATCACGCCGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCCT 480
        |||
Db    421 GAAGCAGTGGGAATCACGCCGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCCT 480
        |||

Qy    481 TCCTCCATCCATGAGACCGTTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAG 540
        |||
  
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Db      481  TCCTCCATCCATGAGACCGTTTTTTGAAAATGACGGGATCCCATCAGACTGATCGATCAG 540
Qy      541  ATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCGTTGAAGGACGCCATCAGC 600
Db      541  ATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCGTTGAAGGACGCCATCAGC 600
Qy      601  AGGCTGAGCGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAG 660
Db      601  AGGCTGAGCGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAG 660
Qy      661  TCTGAGGTAGCAGAGCGTCTAGGGATTTGCGAGGTCAGGTCTCGGCTCTGGAAAAGCGT 720
Db      661  TCTGAGGTAGCAGAGCGTCTAGGGATTTGCGAGGTCAGGTCTCGGCTCTGGAAAAGCGT 720
Qy      721  ATCCTGCTAACGATCAAGGAGCAAATTGAACATTAG 756
Db      721  ATCCTGCTAACGATCAAGGAGCAAATTGAACATTAG 756

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RESULT 3

BACSPQI

LOCUS BACSPQI 1746 bp DNA linear BCT 16- OCT- 1997
 DEFINITION Paenibacillus polymyxa spoliAA, spoliAB, and sigma factor genes,
 complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

FEATURES

source

-35_signal

-10_signal

gene

CDS

gene

CDS

gene

CDS

gene

CDS

gene

CDS

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gene

CDS

Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:1406"
 /clone_lib="DSM86"
 6..11
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 details recorded"
 29..33
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 details recorded"
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 details recorded"
 /codon_start=1
 /transl_table=11
 /protein_id="AAB81184.1"
 /db_xref="GI:2529265"
 /translation="MNLQ EMEHHRGVLI VRLSGELDHHTSDM/RMQMDEAI QRRQCE
 HILVLSLKNLQFMDSGLGVLGRYKLI NQKGEMAVCDVNPVHRLLDMSGLFKI MPI
 YDNEVNALTELVVS"
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 details recorded"
 /codon_start=1

CDS

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/translation="MREGTGNNFMSLQFAAKSENEAFARVAVAAFI SRLDPTMDELSD
LKTWVSEAVTNSI HGYDSDPSGVVTI KVGI EADVI TLVVEDAGRG EDLELAKQPLY
TSKPELERSGMGFTI MENFMDEF EAVSEPGGTSVRMKKRI ESKKALYN"
887..1642
/inference="non-experimental evidence, no additional
details recorded"
/codon_start=1
/translation="MEAGGKKTSHSYLEDTEVKRLI ALSQSGNDARETLI NSNI RLV
WSVWQRFMNRGYEPDDL FQ GCI GL LKSVDFDL SYEVKFSTYAVPM I GEI QRFLRD
DGT LKVSRLKETANKVRKMKDEL SKPLNRLPTVKEVADEL GVT PEDVWF AQEANKPP
TSI HETVFENDGDI TLMQI ADESQERWFDKLALNEAI DGLSERERLI VYLYRYRDQ
TQSEVASRLGI SQVQVSRLEKKI LQQI RDQI AQ"

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ORIGIN

Query Match 48.4% Score 366.2; DB 14; Length 1746;
 Best Local Similarity 67.8% Pred. No. 5.2e-106;
 Matches 512; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

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Qy      61  TTGATAGCCAAGAGCCAAGCTGCGGATACGGATGCACGTGAGCTTCTCGTGAATAGCAAT 120
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Db      947 CTTATGCACTGAGTCAATCTGGTGATAATGATGCTCGTGAGACACTAATCAATAGTAAT 1006
Qy      121  ATCAGACTGGTCTGGTCCGTGCGGCTTTATCAACCGCGGGTATGAAGCGGATGAT 180
      |||||
Db     1007 ATCCGGCTCGTCTGGTCTGTCGTGCAGGCTTTATGAACCGGGGTATGAACCTGACGAT 1066
Qy      181  TTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACAAGTTCGATCTTTTCGTAC 240
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Db     1067 CTTTTTCAAATTGGTTCATCGGATTGTTAAAATCGGTGGATAAATTGATCTCAGCTAC 1126
Qy      241  GATGTGAGATTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCAACGCTTTTTTG 300
      |||||
Db     1127 GAAGTGAAGTTCCTACATATGCAGTACCAATGATTATTGGTGAGATTCAACGCTTCCTT 1186
Qy      301  CCGGATGACGGTACGGTTAAGGTGAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGG 360
      |||||
Db     1187 CGAGACGATGGTACTCTCAAGTTAGCGTTCCTTGAAGGAAACAGCCAATAAGGTGCGC 1246
Qy      361  CGATCAAAGGATGAATTGTACAAGCAATTCGGCGGTGCCCCACGATCGCAGAAAGTGGCA 420
      |||||
Db     1247 AAAATGAAGGACGAGCTGTCAAAACCGCTCAATCGCTGCTACAGTCAAGGAGGTTGCT 1306
Qy      421  GAAGCAGTGGGAATCAOGCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGGCGCT 480
      |||||
Db     1307 GATGAGCTGGGAGTGACACGGGAGGATGTTGTTTTGCGCAGGAGGCCAATAAGCCACCT 1366
Qy      481  TCCTCCATCCATGAGACCGTTTTTTGAAAATGACGGGATCCCATCACACTGATCGATCAG 540
      |||||
Db     1367 ACCTCCATTCAAGAAACAGTGTTTGAAAATGACGGGAGACCGATTACACTTATGGATCAG 1426
Qy      541  ATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGC 600
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Db     1427 ATTGCCGACGAATCGCAGGAAAGATGGTTCGACAAGCTGGCGCTGAATGAGGCCATTGAC 1486
Qy      601  AGGCTGAGGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAG 660
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Qy      661 TCTGAGGTAGCAGAGCGTCTAGGGATTTGCGAGGTCAGGTCTCGGGTCTGGAAAAGCGT 720
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Qy      721 ATCCTGCTAACGATCAAGGAGCAAATTGAACATTA 755
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Db      1607 ATTTTACAACAGATCCGCGATCAGATTGCCAATA 1641
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RESULT 4

Z54161

LOCUS Z54161 1799 bp DNA linear BCT 18-APR-2005

DEFINITION B. coagulans genes for SpoIIAA, SpoIIAB and sigma factor.

ACCESSION Z54161

VERSION Z54161.1 GI:1552541

KEYWORDS sigma factor; SpoIIAA; SpoIIAB.

SOURCE Bacillus coagulans

ORGANISM Bacillus coagulans

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE 1 (bases 1 to 1799)

AUTHORS Park, S. G. and Yudkin, M. D.

TITLE Nucleotide sequence of the Bacillus coagulans homologue of the spoIIA operon of Bacillus subtilis

JOURNAL Gene 177 (1-2), 275-276 (1996)

PUBMED 8921882

REFERENCE 2 (bases 1 to 1799)

AUTHORS Park, S. S.

TITLE Direct Submission

JOURNAL Submitted (08-SEP-1995) Sung Goo SG Park, Microbiology Unit, Biochemistry, University of Oxford, South Parks Road, Oxford, OX1 3QU, UK

FEATURES

source

Location/Qualifiers

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/mol_type="genomic DNA"

/isolate="DSM"

/db_xref="taxon:1398"

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75..80

-10_signal

98..101

CDS

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/translation=11

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/db_xref="GOA:P70877"

/db_xref="InterPro:IPR002645"

/db_xref="InterPro:IPR003658"

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CDS

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/translation=11

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/db_xref="InterPro:IPR013325"
/db_xref="UniProtKB/TrEMBL:P70879"
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VWSVVHRLNRYEPDDLFIQI GCI GLLKSVDFDLSDYDKFSTYAVPM I GEI QRFLR
DDGTVKVSRSLKETGNRI RKI RDELTKKLGRSPTVHEI ASELGMPVEEVVMAQEAGKA
PSSI HETVYENDGDPI TLLDQI SDQNDQKWFQI ALQEI RGLEERERLI VYLRYKYD
QTQSEAGERLGI SQVQVSRLEKKI LRVMKERIVEL"

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ORIGIN

Query Match 48.0% Score 363.2; DB 14; Length 1799;
 Best Local Similarity 69.4% Pred. No. 4.9e-105;
 Matches 494; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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Qy      44  ATGACCAAGTGAAAGATTTGATAGCCAAGAGCCAAGCTGGCGATACGGATGCACGTGAGC 103
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Db      990  ATGAGGAAGTGAAAAAOCCTGATCAGGCGCACCGAGGAAGGCGACAGGAGGCACGGGACC 1049
      |||||
Qy      104  TTCTCGTGAATAGCAATATCAGACTGGTCTGGTCCGTCTGTCACGCGCTTTATCAACCGCG 163
      |||||
Db     1050  TGATCGTTGAAAAAATATCCGCTTGTCTGGTCCGTCTGTCACCGCTTTTTAAACCGGG 1109
      |||||
Qy      164  GGTATGAAGCGGATGATTTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACA 223
      |||||
Db     1110  GATATGAACCGGATGACTTATTTCAAATCGGCTGTATCGGGCTGTTAAATCGGTTGATA 1169
      |||||
Qy      224  AGTTCGATCTTTTCGTACGATGTGAGATTTTCGACCTATGCGGTGCCAATGATCATCGGAG 283
      |||||
Db     1170  AATTTGATCTTTTCGTATGATGTCAAATTTTCCACCTATGCAGTCCCATGATCATCGGGG 1229
      |||||
Qy      284  AAATTCACCGCTTTTTTGGCGATGACGGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAA 343
      |||||
Db     1230  AAATCCAGCGGTTTTTGGCGATGACGGGACGGTAAAGGTGAGCCGTTCTTTGAAAGAAA 1289
      |||||
Qy      344  CAGCGAATAAGGTGCGGCGATCAAAGGATGAATTGTACAAGCAATTCCGCCGTGCCCCCA 403
      |||||
Db     1290  CCGGCAACCGGATCCGCAAAATCCGCGATGAGTTAACGAAAAAGCTGGGAGATCGCGGA 1349
      |||||
Qy      404  CGATCCAGAAAGTGGCAGAAGCAGTGGGAATCACGCCGAGGAAGTAGTCTTTGCGCAAG 463
      |||||
Db     1350  CCGTGCATGAAATTGCATCAGAACTCGGATGCCGGTGGAAGAAAGTCGTATGGGCGAGG 1409
      |||||
Qy      464  AGGCAAGCAGAGCGCCTTCTCATCATGAGACCGTTTTTTGAAAAATGACGGCGATCCCA 523
      |||||
Db     1410  AGGCAGGCAAAAGCCCCATCATCTATCCATGAGACGGTATATGAAAAAGATGGGACCCGA 1469
      |||||
Qy      524  TCACACTGATCGATCAGATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCT 583
      |||||
Db     1470  TCAAGCTTCTTGACAGATTTTCAAGCAGAACGACAGAAAGTGGTTTGACAGATTGCCC 1529
      |||||
Qy      584  TGAAGGACGCCATCAGCAGGCTGAGCGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATT 643
      |||||
Db     1530  TCCAGGAAGCGATCAGAGGGCTTGAGGAACGCGAAAGGCTGATTGTGTACCTCCGCTATT 1589
      |||||
Qy      644  ACAAGGATCAGACACAGTCTGAGGTAGCAGAGCGTCTAGGGATTTCCAGGTCCAGGTCT 703
      |||||
Db     1590  ACAAAGACCAGACACAGTCCGAAGCTGGCGAACGGCTTGCATTTCCAGGTGCAGGTTT 1649
      |||||
Qy      704  CCGCTCTGAAAAAGCGTATCCTGCTAACGATCAAGGAGCAAATTGAACATTA 755
      |||||

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Db 1650 CACGGCTTGAAAAGAAAATACTTCGAGTGATGAAAGAGCGCATGGAATTGTA 1701

RESULT 5

AJ704768

LOCUS AJ704768 3701 bp DNA linear BCT 10-MAY-2005
 DEFINITION *Bacillus amyloliquefaciens* dacF gene, spoIIA operon and spoVAA gene (partial), strain FZB42.

ACCESSION AJ704768

VERSION AJ704768.1 GI:63146678

KEYWORDS anti-sigma F factor antagonist; anti-sigmaF factor; dacF gene; penicillin binding protein; sigF gene; Sigma F; spoIIAA gene; spoIIAB gene; spoVAA gene; Stage V sporulation protein AA.

SOURCE *Bacillus amyloliquefaciens* FZB42ORGANISM *Bacillus amyloliquefaciens* FZB42Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1

AUTHORS Stragier, P.

TITLE Comparison of early sporulation genes in *Bacilli* and *Clostridia*

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3701)

AUTHORS Borriess, R.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2004) Borriess R., Biology, Humboldt University, Chaussee Strasse 117, D-10115, GERMANY

COMMENT spoIIA operon 1290 - 3083.

FEATURES

source

Location/Qualifiers

1..3701

/organism="Bacillus amyloliquefaciens FZB42"

/mol_type="genomic DNA"

/strain="FZB42"

/isolation_source="soil"

/db_xref="taxon:326423"

/country="Germany: Berlin-Brandenburg"

gene

123..1292

/gene="dacF"

CDS

123..1292

/gene="dacF"

/EC_number="3.4.16.4"

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/codon_start=1

/translation=11

/product="penicillin binding protein"

/protein_id="CAG28930.1"

/db_xref="GI:63146679"

/db_xref="GOA:Q50J84"

/db_xref="HSSP:P39042"

/db_xref="InterPro:IPR001967"

/db_xref="InterPro:IPR012338"

/db_xref="InterPro:IPR012907"

/db_xref="UniProtKB/TrEMBL:Q50J84"

/translation="MKRLI STLLI GLLTASAPSAFAKPDGKHTSELAHEAKSAVLI E
 RDTGSI LYNKNSRERLAPASMTKI MTMLLI MEALDKGKI KMSDKVVRTSEHAASMGGSQ
 I FLEPGEEMTVKEMLKGI AASGNDASVMAEYI AGSEEDFVSRMKNKAKELGLKDT S
 FKNPTGLPEKDHYSAYDMAKMAKELLKYDKI TQFTGTIEDYLRENTDKKFWLVNTNR
 LI KFYPGVDGKVTGFTGEAKYCLTATAKKGNI RVI AVVFGASTPKERNAQVT KMLDYA
 FSQFKTHPLYKRDQI VGTVKVKKGKQKLI KLTTSEPI SLLAKKGENMDKVKKEVKI NG
 NVTAPVKKGEVLGSLVLKKDGKVL VESPVTA KDDMEKAGFLTFLKRTMGDWTKFK"

operon

1290..3083

/operon="spoIIA"

/function="expression of early forespore genes"

gene

1388..1741

/gene="spoIIAA"

/operon="spoIIA"

CDS

1388..1741

/gene="spoIIAA"

/operon="spoIIA"

/function="binding to SpoIIAB in the presence of ADP"

selectively in the forespore"
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/transl_table=11
/product="anti-sigma F factor antagonist"
/protein_id="CAG28931.1"
/db_xref="GI:63146680"
/db_xref="HSSP:P10727"
/db_xref="InterPro:IPR002645"
/db_xref="InterPro:IPR003658"
/db_xref="UniProtKB/TrEMBL:Q50J83"
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EQSEQKALLTLGVAS"
1738. . 2178
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/operon="spolIA"
1738. . 2178
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/operon="spolIA"
/EC_number="2.7.1.37"
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septation"
/codon_start=1
/transl_table=11
/product="anti-sigmaF factor"
/protein_id="CAG28932.1"
/db_xref="GI:63146681"
/db_xref="GOA:Q50J82"
/db_xref="HSSP:Q32727"
/db_xref="InterPro:IPR003594"
/db_xref="InterPro:IPR010194"
/db_xref="UniProtKB/TrEMBL:Q50J82"
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SEAVTNAIHGYEENCDDGKVYISVTLEDHVVYLTIRDEGIGITDLEEARQPLFTTKPE
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2190. . 2957
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/operon="spolIA"
2190. . 2957
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/operon="spolIA"
/function="sporulation specific sigma factor"
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/transl_table=11
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/db_xref="InterPro:IPR007624"
/db_xref="InterPro:IPR007627"
/db_xref="InterPro:IPR007630"
/db_xref="InterPro:IPR013325"
/db_xref="UniProtKB/TrEMBL:Q50J81"
/translati on="MDVEVKKNSKNAQLKDEHVKELIKKSQEGDQQARDLLIEKNMRL
VWSVVQRFLNRGYEPDDLFGIGIGLLKSVDFDLSDYDVRVSTYAVPMIGEIQRFIR
DDGTVKVSRSLKELGNKIRRAKDELSKTYGRVPTVQEIADHLEIDAEDVVLAEAVRA
PSSI HETVYENDGDPI TLLDQIADHSEEKWFDKIALKEAISDLEEREKLI VYLRYKDK
QTQSEVAERLIGISQVQVSRLEKKILKQIKVQMDHTES"
3084. . >3701
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3084. . >3701
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/codon_start=1
/transl_table=11
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/db_xref="UniProtKB/TrEMBL:Q50J80"
 /translation="MERRI FLRLRHRVKAHTGDIITI GDAAGI AGQCKLKKKLSALPL
 YKVTKKDKNI VVLDI I KVLKTI HTAFPALDVQTVGGAETI VEI HYQKKQLSAVLVGV
 WLLFI GSCLAI MNFHEDVSMREVHI ALYEI I TGERNEYPYLLQI PYSI GLGLGM VF
 FNHI FKKRLNEEPSLEVEMFNQLDL DHYVAMHENEETMKDLHDR'

ORIGIN

Query Match 47.8% Score 361.6; DB 14; Length 3701;
 Best Local Similarity 67.9% Pred. No. 1.8e-104;
 Matches 505; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

Qy	10	GATATCAAAATGOGAGTCAOCCATTTCTGACCAATGACCAAGTGAAAGATTTGATAGCC	69
Db	2202	GTTAAGAAAAACAGCAAAAACGCGCAGCTCAAGGAOCATGAAGTCAAAGAATTAATCAAA	2261
Qy	70	AAGAGCCAAGCTGGCGATAOGGATGCACGTGAGCTTCTCGTGAATAGCAATATCAGACTG	129
Db	2262	AAGAGCCAAGAGGGCGACCAAGCAGGCAAGAGACCTCCTCATAGAAAAAACATGCGTCTT	2321
Qy	130	GTCTGGTCCGTCTGTCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGATTTGTTTCAG	189
Db	2322	GTCTGGTCCGTCTGTTCAAAGGTTCTTAACAGAGGCTATGACCGGATGATCTGTTTCAG	2381
Qy	190	ATCGTTTGCATTGGCTTGCTCAAGGCGCTTGACAAGTTCGATCTTTGTAAGATGTGAGA	249
Db	2382	ATCGGCTGTATCGGATTGTTAAAATCGGTTGATAAATTGATTTGTCTATGATGTCCGT	2441
Qy	250	TTTTGCACCTATGOGGTGCCAATGATCATCGGAGAAATTCACCGCTTTTTGCGGATGAC	309
Db	2442	TTTTCAACTTATGCGGTGCCGATGATTATCGGAGAAATCCACCGCTTCATCCGCGATGAC	2501
Qy	310	GGTACGGTTAAGGTGAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGGCGATCAAAG	369
Db	2502	GGAACCGTCAAAGTTTCAAGATCTTTAAAAGAGCTCGGCAATAAAATACGCGGGGCGAAA	2561
Qy	370	GATGAATTGTACAAGCAATTCGGCGGTGCCCGACGATCGCAGAAAGTGGCAGAAGCAGTG	429
Db	2562	GATGAAGTGTCAAAAACATACGGAAGAGTGCCGACCGTCCAGGAAATCGCGGACCATTTA	2621
Qy	430	GGAATCACGCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCTTCTCTCATC	489
Db	2622	GAAATTGATGCGGAGGATGTGGTGCTTGCGCAGGAAGCGGTGCGGGGCGCTTCATCCATT	2681
Qy	490	CATGAGACCGTTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAGATAGCGGAT	549
Db	2682	CATGAGACCGTGTATGAAAATGACGGAGACCCGATCACCTGCTTGATCAGATGCGCGAT	2741
Qy	550	GAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGCAGGCTGAGC	609
Db	2742	CATTGAGAAGAGAAGTGGTTTGACAAAATCGCCTCAAGGAGGCGATCAGTGATTTGGAA	2801
Qy	610	GAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAGTCTGAGGTA	669
Db	2802	GAACGGGAAAAACTCATTGTCTATCTGAGATATTATAAAGATCAGACACAGTGGGAAGTA	2861
Qy	670	GCAGAGCGTCTAGGGATTTGCGAGGTCCAGGTCTCGCGTCTGAAAAAGCGTATCCTGCTA	729
Db	2862	GCGGAAGCGCTCGGGATTTCCCAAGTCCAGGTATCGAGGCTGGAGAAAAAATATTAAAG	2921
Qy	730	ACGATCAAGGAGCAAATTGAACAT	753
Db	2922	CAGATTAAAGTGCAGATGGATCAT	2945

RESULT 6
 CP000560_22/c
 WPCOMMENT

Sequence split into 40 fragments LOCUS CP000560 Accession CP000560
 Fragment Name Begin End

CP000560_00	1	110000
CP000560_01	100001	210000
CP000560_02	200001	310000
CP000560_03	300001	410000
CP000560_04	400001	510000
CP000560_05	500001	610000
CP000560_06	600001	710000
CP000560_07	700001	810000
CP000560_08	800001	910000
CP000560_09	900001	1010000
CP000560_10	1000001	1110000
CP000560_11	1100001	1210000
CP000560_12	1200001	1310000
CP000560_13	1300001	1410000
CP000560_14	1400001	1510000
CP000560_15	1500001	1610000
CP000560_16	1600001	1710000
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CP000560_32	3200001	3310000
CP000560_33	3300001	3410000
CP000560_34	3400001	3510000
CP000560_35	3500001	3610000
CP000560_36	3600001	3710000
CP000560_37	3700001	3810000
CP000560_38	3800001	3910000
CP000560_39	3900001	3918589

Continuation (23 of 40) of CP000560 from base 2200001 (CP000560 *Bacillus amyloliquefaciens*)

Query Match 47.8% Score 361.6; DB 14; Length 110000;
 Best Local Similarity 67.9% Pred. No. 3.1e-104;
 Matches 505; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

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Qy      10  GATATCAAAATGCGAGTCAACATTTCTGACCAATGACCAAGTGAAAGATTTGATAGCC 69
          |||
Db      47250 GTTAAGAAAAACAGCAAAAACGCGCAGCTCAAGGACCATGAAGTCAAAGAATTAATCAAA 47191
          |||
Qy      70  AAGAGCCAAGCTGCGATACGGATGCACGTGAGCTTCTCGTGAATAGCAATATCAGACTG 129
          |||
Db      47190 AAGAGCCAAGAGGGCGACCAGCAGGCAAGAGACCTCCTCATAGAAAAAACATGCGTCTT 47131
          |||
Qy     130  GTCTGGTCCGTGCTCCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGATTTGTTTCAG 189
          |||
Db     47130 GTGTGGTCCGTGCTTCAAAGGTTCTTAAACAGAGGCTATGAGCCGGATGATCTGTTTCAG 47071
          |||
Qy     190  ATCGGTTGCATTGGCTTGCTCAAGGCCGTTGACAAGTTCGATCTTTGATACGATGTGAGA 249
          |||
Db     47070 ATCGGCTGTATCGGATTGTTAAAATCCGTTGATAAATTGATTTGTCTATGATGTCCGT 47011
          |||
Qy     250  TTTTCGACCTATGCGGTGCAATGATCATCGGAGAAATTCACGCTTTTGGCGGATGAC 309
          |||
Db     47010 TTTTCAACTTATGCGGTGCGGATGATTATCGGAGAAATCCAGCGCTTCATCCGCGATGAC 46951
          |||
Qy     310  GGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGGCGATCAAAG 369
          |||
Db     46950 GGAACCGTCAAAGTTTCAAGATCTTTAAAAGAGCTCGGCAATAAAATACGCCGGGCGAAA 46891
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Qy      370 GATGAATTGTACAAGCAATTCGGCCGTGCCCCACGATCGCAGAAAGTGGCAGAAGCAGTG 429
          |||||
Db      46890 GATGAACTGTCAAAAACATACGGAAGAGTGCCGACCGTCCAGGAAATCGCGGACCATTTA 46831
          |||||
Qy      430 GGAATCACGCCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCTTCTCTCATC 489
          |||||
Db      46830 GAAATTGATGCGGAGGATGTGGTGCTTGCGCAGGAAGGGTGCGGGGCGCTTTCATCCATT 46771
          |||||
Qy      490 CATGAGACCGTTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAGATAGCGGAT 549
          |||||
Db      46770 CATGAGACCGTGTATGAAAATGACGGAGACCCGATCACCGTCTTGATCAGATCGCCGAT 46711
          |||||
Qy      550 GAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGCAGGCTGAGC 609
          |||||
Db      46710 CATTGAGAAGAGAAAGTGGTTTGACAAAATCGCCCTCAAGGAGGCGATCAGTGATTTGGAA 46651
          |||||
Qy      610 GAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAGTCTGAGGTA 669
          |||||
Db      46650 GAACGGGAAAAACTCATTGTCTATCTGAGATATTATAAAGATCAGACACAGTCGGAAGTA 46591
          |||||
Qy      670 GCAGAGCGTCTAGGGATTTGCGAGGTCCAGGTCTCGCGTCTGAAAAGCGTATCCTGCTA 729
          |||||
Db      46590 GCGGAACGGCTCGGGATTTCCCAAGTCCAGGTATCGAGGCTGGAGAAAAAATATTAAAG 46531
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Qy      730 ACGATCAAGGAGCAAATTGAACAT 753
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Db      46530 CAGATTAAAGTGCAGATGGATCAT 46507
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RESULT 7

CP000813_21/c

WPCOMMENT

Sequence split into 37 fragments LOCUS CP000813 Accession CP000813

Fragment Name	Begin	End
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CP000813_02	200001	310000
CP000813_03	300001	410000
CP000813_04	400001	510000
CP000813_05	500001	610000
CP000813_06	600001	710000
CP000813_07	700001	810000
CP000813_08	800001	910000
CP000813_09	900001	1010000
CP000813_10	1000001	1110000
CP000813_11	1100001	1210000
CP000813_12	1200001	1310000
CP000813_13	1300001	1410000
CP000813_14	1400001	1510000
CP000813_15	1500001	1610000
CP000813_16	1600001	1710000
CP000813_17	1700001	1810000
CP000813_18	1800001	1910000
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CP000813_28	2800001	2910000
CP000813_29	2900001	3010000
CP000813_30	3000001	3110000
CP000813_31	3100001	3210000
CP000813_32	3200001	3310000
CP000813_33	3300001	3410000

CP000813_34 3400001 3510000
 CP000813_35 3500001 3610000
 CP000813_36 3600001 3704465

Continuation (22 of 37) of CP000813 from base 2100001 (CP000813 *Bacillus pumilus* SAFR-

Query Match 46.9% Score 354.6; DB 14; Length 110000;
 Best Local Similarity 67.6% Pred. No. 5.6e-102;
 Matches 498; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

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Qy      16  AAAAAATGCGAGTCAACCATTTCTGACCAATGAOCCAAGTGAAAGATTTGATAGCCAAGAGC 75
      |||
Db      14501 AAGCAAGCAAAAAAAGCCCAGCTGTCAAATGATGAAGTCAAAGAGCTCATCAAAAAAAGC 14442
      |||
Qy      76  CAAGCTGGCGATAOCCGATGCAOCTGAGCTTCTCGTGAATAGCAATATCAGACTGGTCTGG 135
      |||
Db      14441 CAAGACGGTGATCAGCAAGCAAGAGACCTCCTCGTAGAAAAAACATGOGTCTTGTTTGG 14382
      |||
Qy     136  TCCGTCTGCCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGATTTGTTTCAGATCGGT 195
      |||
Db     14381 TCCGTTGTTTCAGCGCTTTTTAAATAGAGGATATGAACCAGATGATTTGTTTCAAATTGGC 14322
      |||
Qy     196  TGCATTGGCTTGCTCAAGGCGGTTGACAAGTTCGATCTTTCTGACGATGTGAGATTTTCG 255
      |||
Db     14321 TGTATTGGATTGCTAAAATCCGTTGATAAATTTGATTTGTATATGATGTGAAGTTTTTCG 14262
      |||
Qy     256  ACCTATGCGGTGCCAATGATCATCGGAGAAATTCACCGCTTTTTGCGCGATGACGGTACG 315
      |||
Db     14261 ACCTATGCTGTTCCAATGATTATTGGTGAAATCCAGCGATTCAATTCGGGATGATGGAACA 14202
      |||
Qy     316  GTTAAGGTCAGTGATCGTTAAAAGAAACAGCGAATAAGGTCCGCGCATCAAAGGATGAA 375
      |||
Db     14201 GTCAAAGTCAGCCGGTCACTAAAGGAACTCGGAAATAAAATCCGCGCGGCAAGAGATGAA 14142
      |||
Qy     376  TTGTACAAGCAATTCGGCCGTGCCCCACGATCGCAGAAGTGGCAGAAGCAGTGGGAATC 435
      |||
Db     14141 TTGTCTAAGTCTCATGGAAGAATGCCGACCGTCCAGGAAATAGCCGAATATCTAGATATC 14082
      |||
Qy     436  ACCCGCGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCCTTCTCCATCCATGAG 495
      |||
Db     14081 ACAOCAGAGGATGTGTCCTCGGCCAAGAAGCGGTCCGAAOCCGCTGTCGATTGATGAA 14022
      |||
Qy     496  ACGTTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAGATAGCGGATGAAGGT 555
      |||
Db     14021 ACGGTTTATGAAAATGATGGGGACCCCATACATTACTCGATCAAATTGCTGATCATTCA 13962
      |||
Qy     556  GTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGCAGGCTGAGCGAGCGT 615
      |||
Db     13961 GAAGAAAGATGGTTTGATAAAATCGCGCTGAAAGAAGCGATCAAGGAATTAGAAGAAOCA 13902
      |||
Qy     616  GAGCAGCTCATGCTCTACCTGCGCTATTACAAGGATCAGACACAGTCTGAGGTAGCAGAG 675
      |||
Db     13901 GAAAAACTCATTGTGTACTTAAGGTATTATAAAGACCAAAACACAATCTGAGGTAGCAGAG 13842
      |||
Qy     676  CGTCTAGGGATTTGCGAGGTCCAGGTCTCGCGTCTGGAAAAGCGTATCCTGCTAAGCATC 735
      |||
Db     13841 AGACTCGGCATTTACAAGTACAAGTCTCGCGGCTCGAAAAGAAAATTTTAAACAAATC 13782
      |||
Qy     736  AAGGAGCAAATTGAACA 752
      |||
Db     13781 CAAATGCAAATGGATCA 13765
  
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RESULT 8

CP000557_23/c

WPCOMMENT

Sequence split into 36 fragments LOCUS CP000557 Accession CP000557

Fragment Name	Begin	End
CP000557_00	1	110000
CP000557_01	100001	210000

CP000557_02	200001	310000
CP000557_03	300001	410000
CP000557_04	400001	510000
CP000557_05	500001	610000
CP000557_06	600001	710000
CP000557_07	700001	810000
CP000557_08	800001	910000
CP000557_09	900001	1010000
CP000557_10	1000001	1110000
CP000557_11	1100001	1210000
CP000557_12	1200001	1310000
CP000557_13	1300001	1410000
CP000557_14	1400001	1510000
CP000557_15	1500001	1610000
CP000557_16	1600001	1710000
CP000557_17	1700001	1810000
CP000557_18	1800001	1910000
CP000557_19	1900001	2010000
CP000557_20	2000001	2110000
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CP000557_28	2800001	2910000
CP000557_29	2900001	3010000
CP000557_30	3000001	3110000
CP000557_31	3100001	3210000
CP000557_32	3200001	3310000
CP000557_33	3300001	3410000
CP000557_34	3400001	3510000
CP000557_35	3500001	3550319

Continuation (24 of 36) of CP000557 from base 2300001 (CP000557 *Geobacillus thermodeni*)

Query Match 46.8% Score 353.6; DB 14; Length 110000;
 Best Local Similarity 68.9% Pred. No. 1.2e-101;
 Matches 485; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

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Qy      53  TGAAGATTGATAGCCAAGAGCCAAGCTGGCGATACGGATGCACGTGAGCTTCTCGTGA 112
      |||||
Db 58581  TGAAGGAGCTGATCGGCCGAGTCAGGAAGGCGACCAAGAACCCCGCGATGAAATTATTG 58522
      |||||
Qy     113  ATAGCAATATCAGACTGGTCTGGTCCGTCCAGCGCTTTATCAACCGCGGGTATGAAG 172
      |||||
Db 58521  AAAAAAATATGCGCCTCGTCTGGTCCGTCCAGCGTTTCTTAAATCGTGGCTATGAAG 58462
      |||||
Qy     173  CCGATGATTTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACAAGTTTCGATC 232
      |||||
Db 58461  CCGATGATTTGTTCCAAATCGGCTGCATCGGCTTGTTAAAATCAGTCGATAAGTTTGACT 58402
      |||||
Qy     233  TTTGATACGATGTGAGATTTTGGACCTATGCGGTGCCAATGATCATCGGAGAAATCAAC 292
      |||||
Db 58401  TATCGTATGACGTCAAGTTTGGACCTACGCGGTGCCGATGATCATCGGGAGATTGAGC 58342
      |||||
Qy     293  GCTTTTTGCGCGATGACGGTACGGTTAAGGTCAGTCGATCGTTAAAAGAAACAGCGAATA 352
      |||||
Db 58341  GATTTCTCGCGATGACGGCAAGGTGAAAGTCAGCGCTCGCTGAAAGAGATGGGCAATA 58282
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Qy     353  AGGTGCGGCGATCAAAGGATGAATTGTACAAGCAATTGCGCGGTGCCCCACGATCGCAG 412
      |||||
Db 58281  AAATCGCAGGAGCAAGGAAGTGTCCAAGACGCGGGGCGGGGCGGCGGCGGCGGCGG 58222
      |||||
Qy     413  AAGTGGCAGAACGAGTGGGAATCAAGCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCA 472
      |||||
Db 58221  AAATCGCGACCATTTGGGTGTTTGGCGGAAGAGTCTTCTCGGCCAAGAGGCGGTTTC 58162
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Db      58161 |GCTCGCGCGGCTCGATCCATGAAACAGTGTATGAAAACGACGGCGATCCGATCAAGCTGC| 58102
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Db      58101 |TCGATCAAATCGCGGATGCTGACGAGGCGTCATGGTTTGAGAAAATTGCCTTAAAAAAG| 58042
Qy      593 |CCATCAGCAGGCTGAGCGAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATC| 652
Db      58041 |CGATTGAAGAGCTCGATGAGCGCGAAAGGCTCATCGTCTATTTGCGTTATTACAAAGACC| 57982
Qy      653 |AGACACAGTCTGAGGTAGCAGAGCGTCTAGGGATTTCCGAGGTCCAGGTCTGCGTCTGG| 712
Db      57981 |AAACCCAGTCCGAAGTGGCAGCAAGACTCGGCATCTCTCAAGTGCAAGTATCCCGGCTGG| 57922
Qy      713 |AAAAGCGTATCCTGCTAACGATCAAGGAGCAAATTGAACATTAG| 756
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RESULT 9

AP006627_19

WPCOMMENT

Sequence split into 43 fragments LOCUS AP006627 Accession AP006627

Fragment Name	Begin	End
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AP006627_02	200001	310000
AP006627_03	300001	410000
AP006627_04	400001	510000
AP006627_05	500001	610000
AP006627_06	600001	710000
AP006627_07	700001	810000
AP006627_08	800001	910000
AP006627_09	900001	1010000
AP006627_10	1000001	1110000
AP006627_11	1100001	1210000
AP006627_12	1200001	1310000
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AP006627_15	1500001	1610000
AP006627_16	1600001	1710000
AP006627_17	1700001	1810000
AP006627_18	1800001	1910000
AP006627_19	1900001	2010000
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AP006627_37	3700001	3810000
AP006627_38	3800001	3910000
AP006627_39	3900001	4010000
AP006627_40	4000001	4110000
AP006627_41	4100001	4210000
AP006627_42	4200001	4303871

Continuation (20 of 43) of AP006627 from base 1900001 (AP006627 *Bacillus clausii* KSM-1)

Query Match 46.1% Score 348.4; DB 14; Length 110000;
 Best Local Similarity 68.2% Pred. No. 5.6e-100;
 Matches 484; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

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Qy      97 OGTGAGCTTCTCGTGAATAGCAATATCAGACTGGTCTGGTCCGTCTGCCAGOGCTTTTATC 156
      |||
Db      12248 OGGGATTGATCGTCAACCATAACACACGTCTCGTCTGGTCAGTCGTCCAAOGTTTTTTTG 12307
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Qy      157 AACCGGGGTATGAAGCGGATGATTTGTTTCAGATCGTTGCATTGGCTTGCTCAAGGCC 216
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Db      12308 AATCGGGTTATGAGGCAGACGACCTTTTTCAAATTGGCTGCATTGGTTTGATTAACTCT 12367
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Qy      217 GTTGACAAGTTGATCTTTTGTACGATGTGAGATTTTGCACCTATGCGGTGCCAATGATC 276
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Db      12368 GTCGACAAATTTGACCTTCTCTATGATGTGAAATTCTCCACGTATGCTGTGCCAATGATT 12427
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Qy      277 ATCGGAGAAATTCACGCTTTTTTGCGCGATGACGGTACGGTTAAGGTGAGTCGATOGTTA 336
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Db      12428 ATTGGGGAAATCCACGTTTTTTGCGGGATGATGGTACGGTGAAAGTAAGCCGGTCCATT 12487
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Qy      337 AAAGAAACAGCGAATAAGGTGCGGGGATCAAAGGATGAATTGTACAAGCAATTCGGCGGT 396
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Qy      397 GCGCCACGATGCGAGAAGTGGCAGAAGCAGTGGGAATCACGCCGAGGAAGTAGTCTTT 456
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Qy      457 GCGCAAGAGGCAAGCAGAGCGCTTCTCCATCCATGAGACCGTTTTTTGAAAATGACGGC 516
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Qy      517 GATCCCATCACACTGATCGATCAGATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAA 576
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Qy      637 CGCTATTACAAGGATCAGACACAGTCTGAGGTAGCAGAGCGTCTAGGGATTTGCGAGGTC 696
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Qy      697 CAGGTCTCGGTCTGGAAAAGCGTATCCTGCTAACGATCAAGGAGCAAAT 746
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RESULT 10
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 LOCUS BACSPQ2A 864 bp DNA linear BCT 26- APR- 1993
 DEFINITION B. subtilis spoliA gene encoding a sporulation-specific sigma factor, complete cds.
 ACCESSION M15744
 VERSION M15744.1 GI:143610
 KEYWORDS sporulation-specific sigma factor.
 SOURCE Bacillus subtilis
 ORGANISM Bacillus subtilis
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 REFERENCE 1 (bases 1 to 864)
 AUTHORS Yudkin, M D.
 TITLE Structure and function in a Bacillus subtilis sporulation-specific sigma factor: molecular nature of mutations in spoliA

JOURNAL J. Gen. Microbiol. 133 (Pt 3), 475-481 (1987)
 PUBMED 3116160
 COMMENT Original source text: B.subtilis (strain 168) DNA, clone
 BglII/PstI.
 Draft entry and clean copy sequence for [1] kindly provided by
 M.D. Yukin, 26-MAY-1987.

FEATURES
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 /mol_type="genomic DNA"
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 /db_xref="taxon:1423"

CDS
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 DDGTVKVSRSLKELGNKIRAKDELSKTLGRVPTVQEIADHLEIEAEDVWLAEAVRA
 PSSIHETVYENDGDPI TLLDQIADNSEEKWFDKIALKEAISDLEEREKLI VYLRYRKD
 QTQSEVAERLGI SQVQVSRLEKKI LKQI KVVQMDHTDG"

ORIGIN 2 bp upstream of ClaI site.

Query Match 45.7% Score 345.6; DB 14; Length 864;
 Best Local Similarity 66.5% Pred. No. 2.1e-99;
 Matches 495; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

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Qy      10  GATATCAAAATGCGAGTCAACATTTCTGACCAATGACCAAGTGAAAGATTTGATAGCC 69
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Db      102 GTTAAGAAAAACGGCAAAAACGCTCAGCTGAAGGATCATGAAGTAAAGGAATTAATCAA 161
      |||
Qy      70  AAGAGCCAAGCTGGCGATAOAGGATGCAOCTGAGCTTCTCGTGAATAGCAATATCAGACTG 129
      |||
Db      162 CAAAGGCCAAATGGCGACCAGCAGGCAAGAGACCTOCTCATAGAAAAAACATGCGTCTT 221
      |||
Qy      130 GTCTGGTCCGTCTGTCAGCGCTTTATCAACCGCGGGTATGAAGCGGATGATTTGTTTCAG 189
      |||
Db      222 GTTTGGTCTGTCTGACAGCGGTTTTTAAACAGAGGATATGAGCCTGACGATCTCTTCAG 281
      |||
Qy      190 ATCGGTTGCATTGGCTTGCTCAAGGCCGTTGACAAGTTCGATCTTTCTGACGATGTGAGA 249
      |||
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      |||
Qy      250 TTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCAACGCTTTTTGCGCGATGAC 309
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Db      342 TTTTCAACGTATGCAGTGCCGATGATTATCGGAGAAATCCAACGATTTATCGGTGATGAC 401
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Qy      310 GGTACGGTTAAGGTGAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGGCGATCAAAG 369
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Db      402 GGAACCGTAAAGGTATCACGGTCATTAAAAGAGCTTGGAAACAAAATCOGGGCGCGGAAG 461
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Qy      370 GATGAATTGTACAAGCAATTGGGCGGTGCCCCACGATCGCAGAAAGTGGCAGAAAGCAGTG 429
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Db      462 GATGAGCTTTGAAAACACTGGGCAGAGTGCCGACGGTGCAGGAGATCGCTGACCATTG 521
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Qy      430 GGAATCACGCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCTTOCTOCATC 489
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Db      522 GAGATTGAAGCTGAGGATGTTGTACTGGCCAAGAGGCGGTAAAGGCTCATCTTCGATT 581
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Qy      490 CATGAGACCGTTTTTAAAATGACGGCGATCCCATCACACTGATCGATCAGATAGCGGAT 549
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Qy 610 GAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAGTCTGAGGTA 669
 Db 702 GAAAGGGAAAACTAATCGTCTATCTCAGATATTATAAAGACCAGACACAGTCCGAGGTG 761
 Qy 670 GCAGAGCGTCTAGGGATTTGCGAGGTCCAGGTCTCGCGTCTGAAAAAGOGTATCCTGCTA 729
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RESULT 11

Z99116/ c

LOCUS Z99116 204537 bp DNA linear BCT 18- APR- 2005
 DEFINITION *Bacillus subtilis* complete genome (section 13 of 21): from 2409151 to 2613687.

ACCESSION Z99116 AL009126

VERSION Z99116.2 GI:32468787

KEYWORDS

SOURCE

ORGANISM

Bacillus subtilis subsp. *subtilis* str. 168*Bacillus subtilis* subsp. *subtilis* str. 168Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE

AUTHORS

1 (bases 1 to 204537)

Kunst, F., Ogasawara, N., Moszer, I., Albertini, A. M., Alloni, G., Azevedo, V., Bertero, M. G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S. C., Bron, S., Brouillet, S., Bruschi, C. V., Caldwell, B., Capuano, V., Carter, N. M., Choi, S. K., Codani, J. J., Connerton, I. F., Cummings, N. J., Daniel, R. A., Denizot, F., Devine, K. M., Dusterhoft, A., Ehrlich, S. D., Emerson, P. T., Entian, K. D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S. Y., Glaser, P., Goffeau, A., Golightly, E. J., Grandi, G., Guiseppe, G., Guy, B. J., Haga, K., Haiech, J., Harwood, C. R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hulio, M. F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Konigstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S. M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Melado, R. P., Mazon, M., Mestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S. H., Parro, V., Pohl, T. M., Portetelle, D., Porwollik, S., Prescott, A. M., Presecan, E., Pujic, P., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadai, Y., Satoh, T., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Seror, S. J., Serron, P., Shin, B. S., Soldo, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Vambutt, R., Wedler, E., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida, K., Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. and Danchin, A.

TITLE

The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*

JOURNAL

Nature 390 (6657), 249-256 (1997)

PUBMED

9384377

REFERENCE

2 (bases 1 to 204537)

AUTHORS

Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

TITLE

Direct Submission

JOURNAL

Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48

COMMENT

On Jul 7, 2003 this sequence version replaced gi:2634723.

This entry contains data from release R16.1 of the SubtiList database. Further data on gene annotation and detailed information about changes from previous releases can be found at <http://genolist.pasteur.fr/SubtiList/>.

FEATURES	Location/Qualifiers
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	LVSQGMKEPVQDVAI QYEGTI AKLETSTFI TKALLSGFLKPRVDSTVNEVNAGGVAKER GI SFSEKI SSSESGYDNCI SVKVTGDRSTFTVTATYI PHFGERI VEI NGFNI DFYPTG HLVYI QHQDTTGVI GRVGR I LGNDI NI ATMQVGRKEKGGEAI MMLSFDRHLEDKI VK ELTNVPDI VSVKLI DLP"
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Query Match 45.7% Score 345.6; DB 14; Length 204537;
 Best Local Similarity 66.5% Pred. No. 4.9e-99;
 Matches 495; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

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Qy	130	GTCTGGTCCGTCTGACAGCGCTTTATCAACCGGGGTATGAAGCGGATGATTTGTTTCAG	189
Db	34103	GTTTGGTCTGTCTGACAGCGGTTTTAAACAGAGGATATGAGCCTGACGATCTCTTCCAG	34044
Qy	190	ATCGGTTGCATTGGCTTGCTCAAGGCGGTTGACAAGTTCGATCTTTCGTACGATGTGAGA	249
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Qy	250	TTTTCGACCTATGCGGTGCCAATGATCATCGGAGAAATTCAACGCTTTTTGCGCGATGAC	309
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Qy	310	GGTACGGTTAAGGTGAGTCGATCGTTAAAAGAAACAGCGAATAAGGTGCGGCGATCAAAG	369
Db	33923	GGAACCGTAAAGGTATCACGGTGATTAAAAGAGCTTGAAACAAAATCGGGGCGCGAAG	33864
Qy	370	GATGAATTGTACAAGCAATTGGGCGGTGCCCCACGATCGCAGAAAGTGGCAGAAGCAGTG	429
Db	33863	GATGAGCTTTGAAAAACACTGGGCAGAGTGCCGACGGTGCAGGAGATCGCTGAOCATTTG	33804
Qy	430	GGAATCACGCGGAGGAAGTAGTCTTTGCGCAAGAGGCAAGCAGAGCGCTTCTCCATC	489
Db	33803	GAGATTGAAGCTGAGGATGTTGTACTGGCCCAAGAGGCGGTAAAGGCTCATCTTCGATT	33744
Qy	490	CATGAGACCGTTTTTTGAAAATGACGGCGATCCCATCACACTGATCGATCAGATAGCGGAT	549
Db	33743	CACGAAACCGTTTTATGAAAATGACGGAGATCCGATTACCTGCTTGATCAAATCGCTGAC	33684
Qy	550	GAAGGTGTGAACAAGTGGTTTGAGAAAATTGCCTTGAAGGACGCCATCAGCAGGCTGAGC	609
Db	33683	AACTCAGAAGAAAAATGGTTTGACAAAATTGCGCTGAAAGAAGCGATCAGCGATTTGGAG	33624
Qy	610	GAGCGTGAGCAGCTCATCGTCTACCTGCGCTATTACAAGGATCAGACACAGTCTGAGGTA	669
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RESULT 12
 BACJH642

LOCUS BACJH642 282700 bp DNA linear BCT 25- MAR- 2006
 DEFINITION Bacillus subtilis DNA, 283 Kb region containing skin element.
 ACCESSION D84432 D82370
 VERSION D84432.1 GI: 2627063
 KEYWORDS LysA; SpoVAF; SpoVAE; SpoVAD; SpoVAC; SpoVAB; SpoVAA; SpoIIAC;
 spoIIAB; SpoIIAA; DacF; YqkO; YqkN; YqkM; YqkL; SpoIIM; YqkK; YqkJ;
 YqkI; AnsB; AnsA; AnsR; YqkH; YqkG; YqkF; YqkE; YqkD; YqkC; YqkB;
 YqkA; YqjZ; YqjY; YqjX; YqjW; YqjV; YqjU; YqjT; YqjS; YqjR; YqjQ;
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 SinR; YqhF; YqhE; YqhD; ComGG; ComGE; ComGD; ComGC; ComGB; ComGA;
 YqhC; YqhB; YqhA; YrkA; YqgZ; YqgY; YqgX; YqgW; YqgV; YqgU; YqgT;
 YqgS; YqgR; YqgQ; YqgP; YqgO; YqgN; YqgM; YqgL; YqgK; YqgJ; YqgI;
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 YqfW; YqfV; YqfU; YqfT; YqfS; YqfR; YqfQ; YqfP; YqfO; YqfN; CccA;
 RpoD; DnaE; YqfM; YqfL; YqfK; YqfJ; YqfI; YqfH; Cdd; DgkA; YqfG;
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 YqeO; YqeN; ComEC; ComEB; ComEA; ComED; YqeM; YqeL; YqeK; YqeJ;
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 SOURCE Bacillus subtilis
 ORGANISM Bacillus subtilis
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 REFERENCE 1
 AUTHORS Mzuno, M., Masuda, S., Takemaru, K., Hosono, S., Sato, T., Takeuchi, M
 and Kobayashi, Y.
 TITLE Systematic sequencing of the 283 kb 210 degrees-232 degrees region
 of the Bacillus subtilis genome containing the skin element and
 many sporulation genes
 JOURNAL Microbiology (Reading, Engl.) 142 (PT 11), 3103-3111 (1996)
 PUBMED 8969508
 REFERENCE 2 (bases 1 to 282700)
 AUTHORS Sato, T.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1996) Tsutomu Sato, Tokyo University of
 Agriculture and Technology, Applied Biological Science; 3-5-8
 Saiwai-cho, Fuchu, Tokyo 183, Japan (E-mail: subtilis@c.tuat.ac.jp,
 Tel: 81-423-67-5706, Fax: 81-423-67-5715)
 COMMENT On or before Jan 7, 1998 this sequence version replaced gi: 1303696,
 gi: 1212727.
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RBS	5797. . 5801
CDS	5809. . 6291

Query Match 45.7% Score 345.6; DB 14; Length 282700;
Best Local Similarity 66.5% Pred. No. 5.2e-99;
Matches 495; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

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RESULT 13

BA000004_16

WPCOMMENT

Sequence split into 42 fragments LOCUS BA000004 Accession BA000004

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BA000004_12	1200001	1310000

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BA000004_14	1400001	1510000
BA000004_15	1500001	1610000
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Continuation (17 of 42) of BA000004 from base 1600001 (BA000004 Bacillus halodurans C

Query Match 45.4% Score 343; DB 14; Length 110000;
 Best Local Similarity 67.3% Pred. No. 3.1e-98;
 Matches 484; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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Qy	398	CCCCACGATCGCAGAAAGTGGCAGAAGCAGTGGGAATCACGCCGAGGAAGTAGTCTTTG	457
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RESULT 15

X63757

LOCUS X63757 1920 bp DNA linear BCT 18- APR- 2005

DEFINITION B. megaterium genes spoIIAA, spoIIAB, spoIIAC, pbp and spoVA.

ACCESSION X63757 S46395

VERSION X63757.1 GI:39650

KEYWORDS pbp gene; spoIIAA gene; spoIIAB gene; spoIIAC gene; spoVA gene.

SOURCE Bacillus megaterium

ORGANISM Bacillus megaterium

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE 1

AUTHORS Tao, Y. P., Hudspeth, D. S. and Vary, P. S.

TITLE Cloning and sequencing of the Bacillus megaterium spoIIA operon

JOURNAL Biochimie 74 (7-8), 695-704 (1992)

PUBMED 1391049

REFERENCE 2 (bases 1 to 1920)

AUTHORS Vary, P. S.

TITLE Direct Submission

JOURNAL Submitted (02-JAN-1992) P. S. Vary, Northern Illinois University,

Dept of Biological Sciences, DeKalb, Illinois 60115-2861, USA

COMMENT On Jun 23, 2005 this sequence version replaced gi:258183.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 44.9% Score 339.6; DB 14; Length 1920;
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Search completed: November 4, 2008, 17:36:32
Job time : 1553 secs

SCORE 3.0